GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT TCTGAGAACATTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA ${\tt CTACTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACC} {\tt ATG} {\tt AAGGAGTATGTG}$ CTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCCTTCACACATCGCACT ATGATGATGAGGACAACTCTCTTTTTCCAACAAGAGGCCCAAGAAGCCATTTTTTCCA TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTCACGAGTTGTACATTGCTC AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT CTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCACAAAGAA GTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAAATACCACTTAATCTTCCCAAAT CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAA GGAATGAATGCTTTACACGTTTTGGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGA GCCAGGGGCATTTGAAGGGGTGACGGTGTTCCATATCAGAATTGCAGAAGCAAAACTGACCT CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAAAAATTTCA ACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT TGGAAAACAATAAACTAAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG AAATGCAACCTGCAACATTTCGTTGTGTTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACTTT GGAATGTAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGAT CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT TAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT CATCTTAAAGTATGATATGATATATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT CTTTATGTTTAAAACTAATTTCTTAAAATAAAGCCTTCAGTAAATGTTCATTACCAACTTGA ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACTCGCATTTT AATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC CACTAACAATTCTACACCAAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAAATCAGAAA ACAGGGAAATTTCATTAAAAATATTGGTTTGAAAT

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<subunit 1 of 1, 379 aa, 1 stop</pre>

<MW: 43302, pI: 7.30, NX(S/T): 1

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

GGCCCCGCCGGCCCGCTGCTCCTCGGGCTGCTGCTCCTCGGCTCCCGGCCCGCCCGCCCGGCCCAGA GAAGGTCTATGCCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTCGGGGTGATGCGCTGCGTGCTGTG CGCCTGCGAGGCGCCTCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACCAGA GTGCCCAACCCCGGCCTGTGGGCAGCCGCCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG CAGTTCGGAGCGGCAGCCGAGCCGCTGTCCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA TGTGGCACTTGTGACACTCACTCACCCTTCAGGGGGGGTCTGGGGGGCCTCTCATCCGGCACCGGGCCCTGGCTGC CAGTGACACAGAGGACTCCTTGCATTTTTTGCTGCTCTTCCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCA ${\tt GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACTC}$ ${\tt GGCCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGGCTCATATGCTGCTGCAGAATGAGCTCTTCCTGAACGT}$ GGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCACGTGGCTGCCCTACTGTGGGCATAGCGCCCG ${\tt AGAGGCCCAGGGTGTGAAGGACCTGGAGCCGGAACTGCTGCGGCACCTGGCAAAAGGCATGGCCTCCCTGAT}$ TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCCTGGGCGGCCCCGAGACCCCAACACATG CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCCACCCGCCCAGCTGCCACACCCGGTGCAGGCTCC TCCCCGGCTGGCCTGTGCCCAGCCTGTGCGTGTCAACCCCACCGACTGCTGCAAACAGTGTCCAGTGGGGTCGGG GGCCCACCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGCTGGGCAGTGGTTCCC AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGCAGG GGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCCTGTGGCTCGGGGAAGGAGTCGATGCTGTTC GGGAGCAGCCAGAGGGCCAAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT GCATTCTCCTGTGGGAAGCCCAGTGCCTTTGCTCCTCTGTCCTGCCTACTCCCACCCCCACTACCTCTGGGAA CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCTGCCCTGCCACCC TCGGCCTCTGTCCTGGAAGCCCCACCCCTTTCCTCCTGTACATAATGTCACTGGCTTGTTGGGATTTTTAATTTA TCTTCACTCAGCACCAAGGGCCCCCGACACTCCACTCCTGCTGCCCCTGAGCTGAGCAGAGTCATTATTGGAGAG

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

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Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242, 390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579, 576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877, 905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCCGCCGTCACTGCG TGCCCGCGCTGGCCCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG AGCCGGACCCGCAGCACCCGGCCGCCGGCGAGCCTGGCTACAGCTGCACCTGCCCCGCCGGGATCTCCGGCG CCAACTGCCAGCTTGTTGCAGATCCTTGTGCCAGCAACCCTTGTCACCATGGCAACTGCAGCAGCAGCAGCAGCA TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCCTGCTACTCAGGAGCCTGACA AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA TGAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC ${\tt GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTCGGCAAGATGCCACTGCCTCACTGATTTTGC}$ TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT CAGGGGGACTGGTCCTCGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACG CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTG AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGCT ${\tt GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTTGCCTTCCTGGTTATACTGGAGAGCTTT}$ GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA CCTGTGCCCAGCTTATTGACTTCTGTGCCCTCAGCCCCTGTGCTCATGGCACGTGCCGCAGCGTGGGCACCAGCT ACAAATGCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA CAAACTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTTGCCGCA TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACTGCCGCAGCATCGACAGCG ${\tt GCCCCATCGCCTATGAAGATTACAGTCCTGATGACAAACCCTTGGTCACACTGATTAAAACTAAAGATTTG}{{\tt TAA}}{\tt T}$ CTTTTTTTGGATTATTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTAAGAAAATAAAAAGCTTAA GAAATTTAAAATGCTAGCTGCTCAAGAGTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG GAAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTTCTGAGTAGAGTTAGGAAAACCAC ${\tt GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTCGTTTTGTGGAAA}$ ${\tt TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCTGATTGAATCTATATTT}$ TTTGTGGCTGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC AAGTCA

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

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Signal sequnce.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365, 375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209, 373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466, 491-503, 529-541, 567-579, 605-617

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTACCT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
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CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
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<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

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TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
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DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA CCCAGGGCCTGCAAGAGCAGGCACGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC AACGACCTGCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCCTGGAG CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCGCTACCTGACGCTC ACCCACACCTGCAACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA CAACATCAGCGGGCTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTCACAG GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG GCTGGAGTGAGGAAGAGCTTCAGGGTGTCCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA GTGGAAAAGGTACAGGAAGAAACAAATGGCAAAGCCCCTTGGAGGACAAGTTCCCGGATGA GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT CAGGCCAGGAACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA GTCTCAGAGTCCTCCCCCCACCCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGA ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC

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><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

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TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
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CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHPDKTHTCPPCPAPELLGGP
SVFLFPPKPKDT

CGCCCAGCGACGTGCGGGCCTGGCCCGCGCCCTCCCGGGCCTGCGTCCCGCGCCC GCCGCCGCCGCCGCCCCAATCCGCGCGGCGCCGCCGCCGTTGCTGCCCCTGCT GCTGCTGCTCTCGGGGGCGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGCGCCGCCTGCCCCC TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT TCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCACGGGGAGACCTTCCTCCACACCA ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCC TGGATGTGGTGACCACGGACCCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAG GACCAGCTGAGCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGGATTTCCTCTTTCAAGCCAA ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA ACCAGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC GGGGCGAGAGCCGAGCTCGGGGCCGGTGCGCCGAGCTCAAGCAGTTCCTGGGCTGCTC AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGAT GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA $\tt CGGCGAGAGGTCCTGCCAGA{\color{red}{TAA}} GCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA$ CGCAGAGGCCGAACCCAAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC CCTCAGCAGGAGCTGGGCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

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WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site. amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224, 300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2. amino acids 325-331

CCCACGCGTCCGCTGGTGTTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGGATGAAATTTCTTCTGGACATCCTC CTGCTTCTCCCGTTACTGATCGTCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCCTAA GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA CATGGACTGGAGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA GGCATTTCTTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG TCTGTGTCCTAATTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA ${\tt AAGCGCAA} \underline{{\tt TAA}} {\tt GCACCTAGTTTTCTGAAAACTGATTTACCAGGTTTAGGTTGATGTCATCTA}$ ATAGTGCCAGAATTTTAATGTTTGAACTTCTGTTTTTTTCTAATTATCCCCATTTCTTCAATA TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAAATGAAGAAAAAGAA CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTTGT TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG

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<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

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Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites. amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

GACTAGTTCTCTTGGAGTCTGGGAGGAGGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG GGGTGACGGCAGGGCAGGGGCCCTGGCCGGGGGAGAAGCGCGGGGGCTGGAGCACCAA CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT ${\tt GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCT}$ TGCTCCTGGGCCTGGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG CGATGGCCGCGACGGCGCGCGCGCCCCGGGGCTCCGGGAGAAAAGGCGAGGGCGGGA GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGGCCGCGAGGAGGCGGGACCCGCGGGG CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC CGAGAGCCGGGTGCCCCCTTGACGCACCCTTGCCCTTCGACCGCGTGCTGAACG AGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA ${\tt CTGGCACAGCTCCCAGTCTTTGCT} \underline{{\tt TAG}} {\tt TGCCCACTGCAAAGTGAGCTCATGCTCACTCC}$ TAGAAGGAGGGTGTGAGGCAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATT GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGCCAAGGAATGGGAAC AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA GAGGAGTGTGCTGCTGGCAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT GGGGTGCTCTCTGGTCCTCTGCTTCTCTGGATCCTCCCCACCCCCTCCTGCTCCTGGG ΑΑΑΑΑΑΑΑΑΑ

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><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

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Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT GCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC CTGAACAGGAAGGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGACTGACCCCAACTGGCTCAAG CCAGGCCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTG CAAGTGGGCTGGAACATGCAGCTGCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCAA CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGGCTCTGTGAGGTCCCC AGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG CCACTGTCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAG TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGC CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCT CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCA GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC ${\tt CCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT}$ $\underline{\textbf{GA}} \textbf{GGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC}$ CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGAGGCCAGGGAGGCCAGGGAGTG AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA TGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAATCAG CTGAAAAAAAAAAAA

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<subunit 1 of 1, 455 aa, 1 stop

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NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICOFAOEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site. amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293, 288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

CGGACGCGTGGGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCT $\tt CGCCCCGCC\underline{\textbf{ATG}} CTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA$ GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC ATCATTTCCCGTTATGCCTTCACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGC GTAAAAGAGAAAAGGAATAAAACCACAGAAGAAAATGGAGAGAGGGGGACTGAAATATTCAG AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCCTTTTTCCTGAGTTATGAGGAGCTTC TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC GCTTCACAACAGCAGGCAGAGGGGCAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCCAT CTACTGTCATTAACCAAAATGAAACATTTGCCAACATAATTTTTAAACCTACTGTAGTACAA CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA AAGACCTTCCTCCTTTACCCAAGAATGTGGTATTCGTGCTTGACAGCAGTGCTTCTATGGTG GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA GGACCGTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGTACATTCACCATATGTCACCCACTGGA GGCACAGACATCAACGGGGCCCTGCAGAGGGCCCATCAGGCTCCTCAACAAGTACGTGGCCCA CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCCTGACGGATGGGAAGCCCACGG TCGGGGAGACGCACACCCTCAAGATCCTCAACAACACCCGAGAGGCCGCCCGAGGCCAAGTC TGCATCTTCACCATTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCG GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCCAGC TCAGTGGTGCAGGCCACCAAGACCCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACCGCCAGCAACA GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGAT CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG AGAAGGAGCGGCTGCGGCAGCCCCAGGCCCTGGCTGTGAGCTACCGCTTCCTCACTCCC CATGTCGGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCGAGGAGCTGGCACGCAGC ${ t CATGGGAGAGATGGTGTTTTTCCTCTCCACCACCTGGGGATACGA{ t TGA}{ t GAAGATGGCCACCT}}$ GCAAGCCAGGAAGACGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGGACCTC

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<subunit 1 of 1, 694 aa, 1 stop</pre>

<MW: 77400, pI: 9.54, NX(S/T): 6

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KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPPLPKNVVFVLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTG
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAGCTACTGAA TCCCAACAGGCAGACCATTTATTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT TGCTGAATTTTCTAGCAGTGAACTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA GGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGT CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG AGCACCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTCATCAATAACCTAAACAAA ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA CCACCACCACCACCACCATCCTTACCATCACAGATTCCCGAGCAGGTGAAGAAGGC TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGGTGGTGGTGGTGCCAT GCTGTGCTTGCTCATCATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACCTATAATCAATGCAGAAGGA ${\sf GGACAGAACAACTCCGAAGAAAAGAAGAGTACTTCATC}$ GAGGTGTCCAACTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

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<subunit 1 of 1, 440 aa, 1 stop</pre>

<MW: 48240, pI: 4.93, NX(S/T): 7

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YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
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AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310, 430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408, 411-417, 427-433, 428-432

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGA $\tt CCGGGACAGAAG{\color{red} ATG} TGCTCCAGGGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTCTTGCCCCT$ GCACTGCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA GCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCCTGCTGCTGCTGC ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG GCGCTGCGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG CAACCTCCACGACCTGGATGTCCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG GCCTCCGGGGCCTGACGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCC GAGGACCTGGCCGGCCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCTGGGTGCGCGAGAGCCACGTCACA CTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT GGAGCTTGACTACGCCGACTTTGGCTGCCCAGCCACCACCACCACCACCACCACCACCACCA CGAGGCCCGTGGTGCGGGAGCCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC CCCACAGCGCCGGCCACTGAGGCCCCCAGCCGCCTCCACTGCCCCACCGACTGTAGGGCC TGTCCCCCAGCCCAGGACTGCCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG GGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGC CAGATGGGGCAGGGCACCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCT GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT AAGCGGCTGGTGACGCTGCGTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG AGGAGGCCTGCGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC CGCGCTGGCTGCGGGGGCAGCCTACTGTGTGCGGCGGGGGGGCCATGGCAGCAGCGG CCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCCAGCGGGTCTGA CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT CTCCCGGAAAGAGCAGAGGGGGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG AAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTAA AATATATATATATATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACTC AGAGACAAGGACTTTGGTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAA ATAAAAAAAAAA

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<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

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Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

 ${\tt TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC}$ ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCCAGTCAGAGAGC CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCCAGCTCTGGGGGGCCGTGGCTTGTGCC ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA GGGGACAGGAGCCCCTCCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC ACCCAAAAACAGAAGCAGCACTCTGTCCTGCACCTGGTTCCCATTAACGCCACCTCCAA AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCCTACAACAGCT GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCATAATTCCCCGG ${\tt GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAAACTG} {\tt TGA} {\tt TT}$ ${\tt GAGCTGAGTATATAAAGGAGGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC}$ $\tt CCCGTTCCTCACTTTCCCTTTTCATTCCCACCCCCTAGACTTTGATTTTACGGATATCTTG$ CTTCTGTTCCCCATGGAGCTCCG

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<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

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Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

CACTTTCTCCCTCTTCCTTTACTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC CCGCCCCCACCCTCTTCTGCACTGCCGTCCTCCGGAAGACCTTTTCCCCTGCTCTGTT TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGAGA TGCTCTAGGGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGGACTGAGGAGCTGC CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGTGACCCCGGTACCTCCATGTACCC GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA CCCAAAGGGCAGAAGGGCTCCATGGGGGGCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC CTTTTCGGTGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTCACCGGCAAGTTCTACTGCTAC GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG ${\tt TGGCTACCTGGTCAAGCACGCCACCGAGCCC} {\tt TAG} {\tt CTGGCCGGCCACCTCCTTTCCTCTCGCC}$ ACCTTCCACCCCTGCGCTGTGCTGACCCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC CCTGGCTTTGGCATTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC GAGACGCGGGTGCGGCAGGGCTCCCAGGGTGCGGCACCGCGGCTCCAGTCCTTGGAAATA ATTAGGCAAATTCTAAAGGTCTCAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGGCAGG AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACTTTCTTGAGGGATAGGTGGACC CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC ${\tt TTCTGTGCCGCCTCCCACACAAATCAGCCCCAGAAGGCCCCGGGGCCTTGGCTTCTGTTTTT}$ TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT CCACGTGTGTTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG CTGGAAGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAGGATTCACTCTCAGGAGC TGGGTGGCAGGAGAGGCAATAGCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCCAGACTCTGATCTCCAGGAACCCC ATAGCCCCTCTCCACCTCACCCCATGTTGATGCCCAGGGTCACTCTTGCTACCCGCTGGGCC CCCAAACCCCCGCTGCCTCTCTTCCTTCCCCCCATCCCCACCTGGTTTTGACTAATCCTGC TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234</pre>

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGCGGATTCGCCGGTCCTTCCCGCGG GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCCTCTCGACGCCA GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAĠAGGGAGGATTAT CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAAACAGCTA GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG CCAAGAGTTACCCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAA TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA CATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA AACCATACCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTA CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGT AGGGAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTTGGTGTCCTGTTCCTGGTGATAGGCC TCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT ${\tt TATTTGATCAATGGGATCTATGTGGACATC} {\tt TAA} {\tt GGATGGAACTCGGTGTCTCTTAATTCATT}$ TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG GCTCTGTTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG GTCTCAAACTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAAATTCAACTGGCTTTTATGCAAA GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATTCTTGGTTCCAGATAAAATCAAC CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410</pre>

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site. amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

GCGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACTGGGA ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAG TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACTCCCTTCCGAAATT GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCCTGAGTAAAT GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA GCCCATATTTGATGAGTATTTTGGGTTTGTTAAACCAATGAACATTTGCTAGTTGTATCA **AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA** AACTAAAATGAATGGAAATTCTTAAAAAAAAAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777</pre>

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125